RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/594,707_

Source: _1Fw P_

Date Processed by STIC: _10/6/06_

ENTERED

IFWP

RAW SEQUENCE LISTING   DATE: 10/06/2006
PATENT APPLICATION: US/10/594,707   TIME: 11:17:33

Input Set : **A:\PTO.RJ.txt**
Output Set: **N:\CRF4\10062006\J594707.raw**

```
 3 <110> APPLICANT: OHARA, Osamu
 4       NAGASE, Takahiro
 5       OISHI, Michio
 6       YOKOTA, Hiroshi
 7       KAMIDA, Osamu
 9 <120> TITLE OF INVENTION: Gene encoding a guanine nucleotide exchange factor and the
gene product
10       thereof
12 <130> FILE REFERENCE: 3190-100
```
C--> 14 <140> **CURRENT APPLICATION NUMBER: US/10/594,707**
```
15 <141> CURRENT FILING DATE: 2006-09-28
17 <150> PRIOR APPLICATION NUMBER: PCT/JP2005/005918
18 <151> PRIOR FILING DATE: 2005-03-31
20 <150> PRIOR APPLICATION NUMBER: JP P2004-106268
21 <151> PRIOR FILING DATE: 2004-03-31
23 <160> NUMBER OF SEQ ID NOS: 27
25 <170> SOFTWARE: PatentIn version 3.1
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 4977
29 <212> TYPE: DNA
30 <213> ORGANISM: Homo sapiens
32 <220> FEATURE:
33 <221> NAME/KEY: misc_feature
34 <223> OTHER INFORMATION: Polynucleotide encoding the protein (SEQ ID NO:2) that have a
fun
35       ction of guanine nucleotide exchange factor.
38 <220> FEATURE:
39 <221> NAME/KEY: CDS
40 <222> LOCATION: (314)..(4336)
43 <220> FEATURE:
44 <221> NAME/KEY: misc_feature
45 <222> LOCATION: (602)..(1126)
46 <223> OTHER INFORMATION: A region encoding Dbl homology domain
49 <220> FEATURE:
50 <221> NAME/KEY: misc_feature
51 <222> LOCATION: (1202)..(1495)
52 <223> OTHER INFORMATION: A region encoding Pleckstrin homology domain
55 <400> SEQUENCE: 1
56 cgctccctcg ctccctcctg ccctcccgct gcagctccgg ctccgctcga cttcctgccg        60
58 ggcgctggca agccgcgcgc tgcctggggt ctccgggggc cgcgcttgca gctggccgag       120
60 tccgggccag ctgaggggct ggcggtgggc gggagcggtc ggcggcctca gcccttcag       180
62 agagcgactt tcaaactcgc gcccgcgtcg cggcagcacc tggcagccc cgcacgccgt       240
64 gcgcgtcccg agcccgcggg gcagctaccg ctcgaatctc cctggggtgc cctccccagg       300
66 cagcaatgcc agg atg cct gtg tcc acc tcc ctc cac cag gat ggc agc        349
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67   Met Pro Val Ser Thr Ser Leu His Gln Asp Gly Ser

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68               1            5                 10
70 cag gag cgg ccg gtg agc ctg acc tct acc acc tcc tcg tcg ggc tcc      397
71 Gln Glu Arg Pro Val Ser Leu Thr Ser Thr Thr Ser Ser Ser Gly Ser
72         15              20              25
74 tcc tgt gac agt cgc agt gcc atg gag gag ccc agc agc tcc gag gct      445
75 Ser Cys Asp Ser Arg Ser Ala Met Glu Glu Pro Ser Ser Ser Glu Ala
76         30              35              40
78 ccc gcc aag aat ggg gca ggc tcc ctg aga agc cgg cat ctg ccc aac      493
79 Pro Ala Lys Asn Gly Ala Gly Ser Leu Arg Ser Arg His Leu Pro Asn
80 45              50              55              60
82 agc aac aac aac tcc agc agc tgg ttg aac gtg aag ggg ccc ctc tcc      541
83 Ser Asn Asn Asn Ser Ser Ser Trp Leu Asn Val Lys Gly Pro Leu Ser
84             65              70              75
86 ccg ttc aac agc cgg gca gcg gca ggg cct gca cac cac aag ctc agc      589
87 Pro Phe Asn Ser Arg Ala Ala Ala Gly Pro Ala His His Lys Leu Ser
88         80              85              90
90 tac ctg ggc cga gtg gtg cgg gag atc gtg gag aca gag cgc atg tac      637
91 Tyr Leu Gly Arg Val Val Arg Glu Ile Val Glu Thr Glu Arg Met Tyr
92         95              100             105
94 gta cag gac ctg cgc agc atc gtg gag gac tac ctc ttg aag atc att      685
95 Val Gln Asp Leu Arg Ser Ile Val Glu Asp Tyr Leu Leu Lys Ile Ile
96     110             115             120
98 gac aca ccc ggg ctg ctg aag cca gaa cag gtc agc gcc ctc ttt ggg      733
99 Asp Thr Pro Gly Leu Leu Lys Pro Glu Gln Val Ser Ala Leu Phe Gly
100 125             130             135                 140
102 aac ata gaa aac atc tac gcg ctg aac agc cag ctc ctc aga gac ctg     781
103 Asn Ile Glu Asn Ile Tyr Ala Leu Asn Ser Gln Leu Leu Arg Asp Leu
104             145             150             155
106 gac agc tgc aat agt gac ccc gtg gct gtg gcc agc tgc ttt gtg gaa     829
107 Asp Ser Cys Asn Ser Asp Pro Val Ala Val Ala Ser Cys Phe Val Glu
108             160             165             170
110 agg agc caa gag ttt gat atc tac act cag tat tgc aac aat tac ccc     877
111 Arg Ser Gln Glu Phe Asp Ile Tyr Thr Gln Tyr Cys Asn Asn Tyr Pro
112         175             180             185
114 aac tcc gtg gcc gcc ctg acg gaa tgc atg cgg gac aag cag cag gcc     925
115 Asn Ser Val Ala Ala Leu Thr Glu Cys Met Arg Asp Lys Gln Gln Ala
116     190             195             200
118 aag ttc ttt cgg gac cgg cag gag ctg cta cag cac tcg ctg ccc ttg     973
119 Lys Phe Phe Arg Asp Arg Gln Glu Leu Leu Gln His Ser Leu Pro Leu
120 205             210             215             220
122 ggc tcc tac ctg ctg aag cca gtc cag cgc atc ctc aag tac cac ctg     1021
123 Gly Ser Tyr Leu Leu Lys Pro Val Gln Arg Ile Leu Lys Tyr His Leu
124             225             230             235
126 ctg ctc cag gaa att gcc aaa cat ttt gat gaa gaa gag gat ggc ttt     1069
127 Leu Leu Gln Glu Ile Ala Lys His Phe Asp Glu Glu Glu Asp Gly Phe
128         240             245             250
130 gag gtg gtg gag gat gcc att gac acc atg acc tgt gtg gcc tgg tac     1117
131 Glu Val Val Glu Asp Ala Ile Asp Thr Met Thr Cys Val Ala Trp Tyr
132         255             260             265
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134 atc aac gac atg aag agg agg cat gag cac gcg gtc cgg ctc cag gag    1165
135 Ile Asn Asp Met Lys Arg Arg His Glu His Ala Val Arg Leu Gln Glu
136     270                 275                 280
138 att cag tca ctc ctc atc aac tgg aag ggg ccc gac ctg acc acc tac    1213
139 Ile Gln Ser Leu Leu Ile Asn Trp Lys Gly Pro Asp Leu Thr Thr Tyr
140 285                 290                 295                 300
142 ggg gag ctt gtc ctg gag ggc aca ttc cgc gtg cat cgc gtg cgc aat    .1261
143 Gly Glu Leu Val Leu Glu Gly Thr Phe Arg Val His Arg Val Arg Asn
144             305                 310                 315
146 gaa agg acc ttt ttc ctc ttt gac aaa aca ctg ctt atc acc aag aag    1309
147 Glu Arg Thr Phe Phe Leu Phe Asp Lys Thr Leu Leu Ile Thr Lys Lys
148             320                 325                 330
150 cgg ggc gat cac ttt gtc tac aag ggc aac atc ccg tgc tcc tcc ctg    1357
151 Arg Gly Asp His Phe Val Tyr Lys Gly Asn Ile Pro Cys Ser Ser Leu
152             335                 340                 345
154 atg ctg atc gaa agc acc aga gac tcc ctg tgc ttc act gtc acc cac    1405
155 Met Leu Ile Glu Ser Thr Arg Asp Ser Leu Cys Phe Thr Val Thr His
156     350                 355                 360
158 tac aag cac agc aag cag cag tac agc atc cag gcc aag aca gtg gag    1453
159 Tyr Lys His Ser Lys Gln Gln Tyr Ser Ile Gln Ala Lys Thr Val Glu
160 365                 370                 375                 380
162 gag aaa cgg aac tgg act cac cac atc aag agg ctc atc cta gag aac    1501
163 Glu Lys Arg Asn Trp Thr His His Ile Lys Arg Leu Ile Leu Glu Asn
164             385                 390                 395
166 cac cat gcc acc att ccc cag aag gcc aag gaa gcc atc ttg gaa atg    1549
167 His His Ala Thr Ile Pro Gln Lys Ala Lys Glu Ala Ile Leu Glu Met
168             400                 405                 410
170 gat tcc tat tat ccc aat cgg tac cgc tgc agc cca gag cgg ctg aag    1597
171 Asp Ser Tyr Tyr Pro Asn Arg Tyr Arg Cys Ser Pro Glu Arg Leu Lys
172             415                 420                 425
174 aag gct tgg tcc tcc cag gat gag gtg tcc acc aat gtg cgc cag ggg    1645
175 Lys Ala Trp Ser Ser Gln Asp Glu Val Ser Thr Asn Val Arg Gln Gly
176     430                 435                 440
178 cgc cgg caa tct gag cca acc aaa cac ctg ctc agg caa ctc aac gag    1693
179 Arg Arg Gln Ser Glu Pro Thr Lys His Leu Leu Arg Gln Leu Asn Glu
180 445                 450                 455                 460
182 aaa gcc cga gca gca gga atg aag cat gca ggc agt gct gga acc ctc    1741
183 Lys Ala Arg Ala Ala Gly Met Lys His Ala Gly Ser Ala Gly Thr Leu
184             465                 470                 475
186 ctg gac ttt ggg cag ccc tcc cgt act cgg ggc ctg cag cca gag gct    1789
187 Leu Asp Phe Gly Gln Pro Ser Arg Thr Arg Gly Leu Gln Pro Glu Ala
188             480                 485                 490
190 gaa ggg gct acc cag gag gag gaa gag gaa gag gag gag gtg gtg gag    1837
191 Glu Gly Ala Thr Gln Glu Glu Glu Glu Glu Glu Glu Glu Val Val Glu
192             495                 500                 505
194 gag gag gag gag gag gag gag gaa gag cag gcc ttt cag gtc tct ctg    1885
195 Glu Glu Glu Glu Glu Glu Glu Glu Glu Gln Ala Phe Gln Val Ser Leu
196     510                 515                 520
198 gag gac ctg aca ggg cat gaa ggc aac gag aag ggg gct ggg ccg gag    1933
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199 Glu Asp Leu Thr Gly His Glu Gly Asn Glu Lys Gly Ala Gly Pro Glu
200 525                 530                 535                 540
202 ccc cca ggc tca gag gag gag gag gag gag cag gag gag agc ctg gcg      1981
203 Pro Pro Gly Ser Glu Glu Glu Glu Glu Glu Gln Glu Glu Ser Leu Ala
204                 545                 550                 555
206 gtg gcg gag cag gta gcc gac ttt gcc agc tcc ctg ctg gcc gcc ctc      2029
207 Val Ala Glu Gln Val Ala Asp Phe Ala Ser Ser Leu Leu Ala Ala Leu
208                 560                 565                 570
210 cac tgc tgg cac tat cgg gcc aac gct tta ctt ttc tcc cgg ggc gct      2077
211 His Cys Trp His Tyr Arg Ala Asn Ala Leu Leu Phe Ser Arg Gly Ala
212             575                 580                 585
214 atg gga aag ggg cgc agg gag tct gaa agc tcc agg agc agc aga agg      2125
215 Met Gly Lys Gly Arg Arg Glu Ser Glu Ser Ser Arg Ser Ser Arg Arg
216         590                 595                 600
218 ccc agt ggc cgg tct cca acc agt act gag aag cgc atg agc ttc gag      2173
219 Pro Ser Gly Arg Ser Pro Thr Ser Thr Glu Lys Arg Met Ser Phe Glu
220 605                 610                 615                 620
222 tcc att tct tcc ctg cca gag gtt gag ccg gac cct gag gct ggg agt      2221
223 Ser Ile Ser Ser Leu Pro Glu Val Glu Pro Asp Pro Glu Ala Gly Ser
224                 625                 630                 635
226 gag caa gag gta ttt tct gct gtg gaa ggg ccc agt gcc gag gag acg      2269
227 Glu Gln Glu Val Phe Ser Ala Val Glu Gly Pro Ser Ala Glu Glu Thr
228                 640                 645                 650
230 cct tca gac aca gaa tct cca gaa gtc ctg gag aca cag ctt gat gcc      2317
231 Pro Ser Asp Thr Glu Ser Pro Glu Val Leu Glu Thr Gln Leu Asp Ala
232             655                 660                 665
234 cac cag ggc ctt ctg ggg atg gac ccc cca ggt gac atg gtg gac ttc      2365
235 His Gln Gly Leu Leu Gly Met Asp Pro Pro Gly Asp Met Val Asp Phe
236         670                 675                 680
238 gtg gca gct gag agc act gag gac ctt aag gcc ctg agc agc gag gag      2413
239 Val Ala Ala Glu Ser Thr Glu Asp Leu Lys Ala Leu Ser Ser Glu Glu
240 685                 690                 695                 700
242 gaa gaa gaa atg gga ggt gcc gcc cag gag cct gag agc ctt ctg cca      2461
243 Glu Glu Glu Met Gly Gly Ala Ala Gln Glu Pro Glu Ser Leu Leu Pro
244                 705                 710                 715
246 ccc tcc gtg ctg gac cag gcc agc gtc att gcg gag cga ttt gtc agc      2509
247 Pro Ser Val Leu Asp Gln Ala Ser Val Ile Ala Glu Arg Phe Val Ser
248             720                 725                 730
250 agc ttc tct cgg cgg agc agc gtg gca cag gag gac agc aag tcc agt      2557
251 Ser Phe Ser Arg Arg Ser Ser Val Ala Gln Glu Asp Ser Lys Ser Ser
252         735                 740                 745
254 ggc ttt ggg agc ccg cgg ctg gtc agc cgg agc agc agc gtg ctc agc      2605
255 Gly Phe Gly Ser Pro Arg Leu Val Ser Arg Ser Ser Ser Val Leu Ser
256         750                 755                 760
258 ctg gag ggc agc gag aag ggc ctg gcc cgg cat ggc agt gcc aca gac      2653
259 Leu Glu Gly Ser Glu Lys Gly Leu Ala Arg His Gly Ser Ala Thr Asp
260 765                 770                 775                 780
262 tcc ctc agc tgt cag ctc tcc cca gaa gtg gac atc agt gtg ggg gtg      2701
263 Ser Leu Ser Cys Gln Leu Ser Pro Glu Val Asp Ile Ser Val Gly Val
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264                785               790               795
266 gcc aca gag gac agc cct tct gtc aat ggg atg gag ccc cca agc cca     2749
267 Ala Thr Glu Asp Ser Pro Ser Val Asn Gly Met Glu Pro Pro Ser Pro
268                800               805               810
270 ggc tgc cca gtg gag cct gac cgg tct tcc tgc aag aag aag gaa tca     2797
271 Gly Cys Pro Val Glu Pro Asp Arg Ser Ser Cys Lys Lys Lys Glu Ser
272            815               820               825
274 gca ctc tcc acc cga gac cgg ctg ttg cta gac aag att aag agc tat     2845
275 Ala Leu Ser Thr Arg Asp Arg Leu Leu Leu Asp Lys Ile Lys Ser Tyr
276        830               835               840
278 tat gaa aat gca gaa cac cat gat gca ggc ttc agc gtc cgt cgc cgg     2893
279 Tyr Glu Asn Ala Glu His His Asp Ala Gly Phe Ser Val Arg Arg Arg
280 845               850               855               860
282 gag agc ctc tcc tac atc ccc aaa gga ctg gta aga aac tcc atc tcc     2941
283 Glu Ser Leu Ser Tyr Ile Pro Lys Gly Leu Val Arg Asn Ser Ile Ser
284                865               870               875
286 agg ttc aac agc ctt ccc cgg cca gac cca gag cca gta cct cca gtg     2989
287 Arg Phe Asn Ser Leu Pro Arg Pro Asp Pro Glu Pro Val Pro Pro Val
288            880               885               890
290 ggg agc aag aga cag gtg ggc tcc cgg ccg act tcg tgg gcc ctg ttt     3037
291 Gly Ser Lys Arg Gln Val Gly Ser Arg Pro Thr Ser Trp Ala Leu Phe
292        895               900               905
294 gag ctc cca gga cca agc cag gca gtc aaa ggg gac cca cct ccc atc     3085
295 Glu Leu Pro Gly Pro Ser Gln Ala Val Lys Gly Asp Pro Pro Pro Ile
296        910               915               920
298 tca gat gct gag ttc cgc cca tct tca gaa att gtg aag atc tgg gag     3133
299 Ser Asp Ala Glu Phe Arg Pro Ser Ser Glu Ile Val Lys Ile Trp Glu
300 925               930               935               940
302 gga atg gag tct tcc gga ggg agc cct ggg aag ggg cca ggc cag ggc     3181
303 Gly Met Glu Ser Ser Gly Gly Ser Pro Gly Lys Gly Pro Gly Gln Gly
304                945               950               955
306 cag gcc aat ggc ttt gac ctg cat gag cca ctc ttc atc ctg gag gag     3229
307 Gln Ala Asn Gly Phe Asp Leu His Glu Pro Leu Phe Ile Leu Glu Glu
308        960               965               970
310 cat gag ctg gga gcc atc aca gag gag tcg gcc act gcc tcc ccg gaa     3277
311 His Glu Leu Gly Ala Ile Thr Glu Glu Ser Ala Thr Ala Ser Pro Glu
312        975               980               985
314 agc tcc tct ccc act gag ggg cgc agc ccg gcc cac  ctg gcc cgg gag    3325
315 Ser Ser Ser Pro Thr Glu Gly Arg Ser Pro Ala His  Leu Ala Arg Glu
316        990               995               1000
318 ctg  aaa gag ctg gtg aag  gag ctg agc agc agt  acc cag ggg gag     3370
319 Leu  Lys Glu Leu Val Lys  Glu Leu Ser Ser Ser  Thr Gln Gly Glu
320 1005              1010              1015
322 ctg  gtg gcc cca ctg cac  ccc cgc atc gtg cag  ctc tcc cac gta     3415
323 Leu  Val Ala Pro Leu His  Pro Arg Ile Val Gln  Leu Ser His Val
324 1020              1025              1030
326 atg  gac agc cac gtg agc  gag cgc gtc aag aac  aag gtc tac cag     3460
327 Met  Asp Ser His Val Ser  Glu Arg Val Lys Asn  Lys Val Tyr Gln
328 1035              1040              1045
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 10/06/2006
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<u>Invalid <213> Response:</u>
**Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.**

Seq#:7,8,9,10,11,12,13,14,15,16,17,18,19

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L:14 M:270 C: Current Application Number differs, Replaced Current Application Number
L:1006 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:1007 M:259 W: Allowed number of lines exceeded, <223> Other Information: